

Nearness to Local Subspace Algorithm for Subspace and Motion Segmentation

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Abstract—There is a growing interest in computer science, engineering, and mathematics for modeling signals in terms of union of subspaces and manifolds. Subspace segmentation and clustering of high dimensional data drawn from a union of subspaces are especially important with many practical applications in computer vision, image and signal processing, communications, and information theory. This paper presents a clustering algorithm for high dimensional data that comes from a union of lower dimensional subspaces of equal and known dimensions. Such cases occur in many data clustering problems, such as motion segmentation and face recognition. The algorithm is reliable in the presence of noise, and applied to the Hopkins 155 Dataset, it generates the best results to date for motion segmentation. The two motion, three motion, and overall segmentation rates for the video sequences are 99.43%, 98.69%, and 99.24%, respectively.

Index Terms—Subspace segmentation, motion segmentation, data clustering.

I. INTRODUCTION

The problem of subspace clustering is to find a nonlinear model of the form $\mathcal{U} = \bigcup_{i \in I} S_i$ where $\{S_i\}_{i \in I}$ is a set of subspaces that is nearest to a set of data $\mathbf{W} = \{w_1, \dots, w_N\} \in \mathbb{R}^d$. The model can then be used to classify the data \mathbf{W} into classes called clusters.

In many engineering and mathematics applications, data lives in a union of low dimensional subspaces [1], [2], [3], [4]. For instance, consider a moving affine camera that captures F frames of a scene that contains multiple moving objects. Let p be a point of one of these objects and let $x_i(p), y_i(p)$ be the coordinates of p in frame i . Define the *trajectory vector* of p as the vector $w(p) = (x_1(p), y_1(p), x_2(p), y_2(p), \dots, x_N(p), y_N(p))^t$ in \mathbb{R}^{2F} . It can be shown that the trajectory vectors of all points of an object in a video belong to a vector subspace in \mathbb{R}^{2F} of dimension no larger than 4 [5], [6]. Thus, trajectory vectors in videos can be modeled by a union $\mathcal{M} = \bigcup_{i \in I} V_i$ of l subspaces where l is the number of moving objects (background is itself a motion). It can also be shown that human facial motion and other non-rigid motions can be approximated by linear subspaces [?], [?]. Another clustering problem that can be modeled as union of subspaces is recognition of faces. Specifically, the set of all two dimensional images of a given face i , obtained under different illuminations and facial positions, can be modeled as a set of vectors belonging to a low dimensional subspace S_i

living in a higher dimensional space \mathbb{R}^d [7], [8], [4]. A set of such images from different faces is then a union $\mathcal{U} = \bigcup_{i \in I} S_i$. Similar nonlinear models arise in sampling theory where \mathbb{R}^d is replaced by an infinite dimensional Hilbert space \mathcal{H} , e.g., $L^2(\mathbb{R}^d)$ [9], [10], [1], [11].

A. Subspace Segmentation Problem

The goal of subspace clustering is to identify all of the subspaces that a set of data $\mathbf{W} = \{w_1, \dots, w_N\} \in \mathbb{R}^d$ is drawn from and assign each data point w_i to the subspace it belongs to. The number of subspaces, their dimensions, and a basis for each subspace are to be determined. The subspace clustering or segmentation problem can be stated as follows:

Let $\mathcal{U} = \bigcup_{i=1}^M S_i$ where $\{S_i \subset \mathcal{H}\}_{i=1}^M$ is a set of subspaces of a Hilbert space \mathcal{H} . Let $\mathbf{W} = \{w_j \in \mathcal{H}\}_{j=1}^N$ be a set of data points drawn from \mathcal{U} . Then,

- 1) determine the number of subspaces M ,
- 2) determine the set of dimensions $\{d_i\}_{i=1}^M$,
- 3) find an orthonormal basis for each subspace S_i ,
- 4) collect the data points belonging to the same subspace into the same cluster.

Note that often the data may be corrupted by noise, may have outliers or the data may not be complete, e.g., there may be missing data points. In some subspace clustering problems, the number M of subspaces or the dimensions of the subspaces $\{d_i\}_{i=1}^M$ are known. A number of approaches have been devised to solve the problem above or some of its special cases.

1) *Sparsity Methods*: Elhamifar *et al.* developed an algorithm for linear and affine subspace clustering using sparse representation of vectors [12], [13]. This method combined with a spectral clustering, gives good results for motion segmentation and it is more general than Eldar's work in compressed sensing [14]. Another method, related to compressed sensing by Liu *et al.* [15], [16] finds the lowest rank representation of the data matrix. The lowest rank representation is then used to define the similarity of an undirected graph, which is then followed by spectral clustering. Favaro *et al.* in [?] extends [12], [13], [15], [16].

2) *Algebraic Methods*: Algebraic methods have also been used for solving the subspace clustering problem. The Generalized Principle Component Analysis (GPCA) is one such method [4], [17], [18], and it can distinguish subspaces of different dimensions. Since it is algebraic, it is computationally inexpensive, however, its complexity increases exponentially

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as the number of subspaces and their dimensions increase. It is also sensitive to noise and outliers. The Robust Algebraic Segmentation is a more specialized algebraic method developed by Rao *et al.* [19] to partition image correspondences to the motions in a 3-D dynamic scene (that contains 3-D rigid body and 2-D planar structures) under perspective camera projection.

3) *Iterative and Statistical Methods*: Iterative methods have also been employed for the subspace clustering problem. For example, the nonlinear least squares [10], [3] and K-subspaces [20] start with an initial estimation of subspaces (or estimation of the bases of the subspaces). Then, a cost function reflecting the “distance” of a point to each subspace is computed and the point is assigned to its closest subspace. After that, each cluster of data is used to reestimate each subspace. The procedure is repeated until the segmentation of data points does not change. These methods, however, are sensitive to the initialization and require a good initial partition for convergence to a global minimum.

The statistical methods such as Multi Stage Learning (MSL) [2], [21] are typically based on Expectation Maximization (EM) [22]. The union of subspaces is modeled by a mixture of probability distributions. For example, each subspace is modeled by a Gaussian distribution. The model parameters are then estimated using *Maximum Likelihood Estimation*. This is done by using a two-step process that optimizes the *log-likelihood* of the model which depends on some hidden (latent) variables. In *E-Step* (Expectation), the expectation of the *log-likelihood* is computed using the current estimate of the latent variables. In *M-Step* (Maximization), the values of the latent variables are updated by maximizing the expectation of the *log-likelihood*. As in the case of the iterative methods, statistical methods highly depends on initialization of model parameters or segmentation and they assume that the number of subspaces as well as their dimensions are known.

The Random Sample Consensus (RANSAC) [23], which has been applied to numerous computer vision problems, is successful in dealing with noise and outliers. But it is a specialized algorithm and assumes that the subspaces have the same dimension and that this dimension is known.

4) *Spectral Clustering Methods*: Spectral clustering [24] is often used in conjunction with other methods as the final step in clustering. Some of the latest subspace clustering algorithms (such as [12], [13], [25]) aim at defining an appropriate similarity matrix between data points which then can be used for further processing using the spectral clustering method. An application of spectral clustering to motion segmentation can be found in [26]. Spectral curvature clustering [27], [28] is a variant of spectral clustering. [?] provides a spectral clustering algorithm that aims at reducing the computational complexity. The motion segmentation algorithm developed by Yan and Pollefeys [29] first estimates a local linear manifold for each trajectory data and then computes an affinity matrix based on the principle subspace angles between each pair of local linear manifolds. The algorithm then uses spectral clustering for segmenting the trajectories of independent, articulated, rigid, and non-rigid body motions. [30] gives a detailed treatment of various related algorithms.

B. Motion Segmentation Problem

The appendix gives a detailed treatment of motion segmentation as a special case of the subspace segmentation problem. First, a data matrix $W_{2F \times N}$ is constructed using N feature points that are tracked across F frames. Then, each column of W (i.e., the trajectory vector of a feature point) is treated as a data point and it is shown that all of the data points that correspond to the same moving object lie in an at most 4-dimensional subspace of \mathbb{R}^{2F} .

C. Paper Contributions

- 1) This paper presents a clustering algorithm for high dimensional data that are drawn from a union of low dimensional subspaces of equal and known dimensions. The algorithm is applicable to the motion segmentation problem and uses some fundamental linear algebra concepts. Some of our ideas are similar to those of Yan and Pollefeys described above in Section I-A.4. However, our algorithm differs from theirs fundamentally as described below:

- Yan and Pollefeys’ method estimate a subspace S_i for each point x_i , and then computes the principle angles between those subspaces as an affinity measure. In our work, we also estimate a subspace for each point, however, these local subspaces are used differently. They are used to compute the distance between each point x_j to the local subspace S_i for the data point x_i .
- In their method, an exponential function for affinity of two points x_i and x_j is used, and this exponential function depends on the principle angles between the subspaces S_i and S_j that are associated with x_i and x_j , respectively. In our case, the affinity measure is different. We first find the distance between x_j and S_i and then apply a threshold, computed from the data, to obtain a binary similarity matrix for all data points.
- The method of Yan and Pollefeys uses spectral clustering on the normalized graph Laplacian matrix of the similarity matrix they propose. However, our approach does not use the spectral clustering on the normalized graph Laplacian of our similarity matrix. Instead, our constructed binary similarity matrix converts our original data clustering problem to a simpler clustering of data from 1-dimensional subspaces which can be solved by any traditional data clustering algorithm.

- 2) Our algorithm is reliable in the presence of noise, and applied to the Hopkins 155 Dataset, it generates the best results to date for motion segmentation. The two motion, three motion, and overall segmentation rates for the video sequences are 99.43%, 98.69%, and 99.24%, respectively.
- 3) Many of the subspace segmentation algorithms use SVD to represent the data matrix W as $W = U\Sigma V^t$ and then replace W with the first r rows of V^t , where r is

the effective rank of W . This paper provides a formal justification for this in Proposition 1.

D. Paper Organization

The organization of the paper is as follows: Section II gives some preliminaries. In Section III, we devise an algorithm for the subspace segmentation problem in the special case where the subspaces have equal and known dimensions. In Section IV, we apply our algorithm to the motion segmentation problem, test it on the Hopkins 155 Datasets, explain the experimental procedure, and present the experimental results.

II. PRELIMINARIES

In this section, we present Proposition 1 which will be used later to justify that a data matrix W whose columns represent data points can be replaced with a lower rank matrix after computing its SVD (i.e. $W = U\Sigma V^t$). It can be paraphrased by saying that for any matrices A, B, C , a cluster of the columns of B is also a cluster of the columns of $C = AB$. A cluster of C however is not necessarily a cluster B , unless A has full rank:

Proposition 1. *Let A and B be $m \times n$ and $n \times k$ matrices. Let $C = AB$. Assume $J \subset \{1, 2, \dots, k\}$.*

- 1) *If $b_i \in \text{span}\{b_j : j \in J\}$ then $c_i \in \text{span}\{c_j : j \in J\}$.*
- 2) *If A is full rank and $m \geq n$ then $b_i \in \text{span}\{b_j : j \in J\} \iff c_i \in \text{span}\{c_j : j \in J\}$*

Proof. The first part can be proved by the simple matrix manipulation

$$\begin{aligned} AB &= A \begin{bmatrix} b_1 & \dots & b_i & \dots & b_k \end{bmatrix} \\ &= \begin{bmatrix} Ab_1 & \dots & Ab_i & \dots & Ab_k \end{bmatrix} \\ &= \begin{bmatrix} Ab_1 & \dots & A \sum_{j \in J} k_j b_j & \dots & Ab_k \end{bmatrix} \\ &= \begin{bmatrix} Ab_1 & \dots & \sum_{j \in J} k_j Ab_j & \dots & Ab_k \end{bmatrix} \\ &= \begin{bmatrix} c_1 & \dots & \sum_{j \in J} k_j c_j & \dots & c_k \end{bmatrix} \end{aligned} \quad (\text{II.1})$$

For the second part, we note that $A^t A$ is invertible and $(A^t A)^{-1} A^t C = B$. We then apply part 1 of the proposition. Note that the same result clearly holds if A is invertible. \square

The proposition above suggest that—for the purpose of column clustering—we can replace a matrix C by matrix B as long as A has the stated properties. Thus by choosing A appropriately the matrix C can be replaced by a more suitable matrix B , e.g. B has fewer rows, is better conditioned or is in a format where columns can be easily clustered.

III. NEARNESS TO LOCAL SUBSPACE APPROACH

In this section, we develop a specialized algorithm for subspace segmentation and data clustering when the dimensions of the subspaces are equal and known. First, a local subspace is estimated for each data point. Then, the distances between the local subspaces and points are computed and a distance matrix is generated. This is followed by construction of a binary similarity matrix by applying a data-driven threshold to the distance matrix. Finally, the segmentation problem is converted to a one-dimensional data clustering problem. The precise steps are described in Algorithm 1 and in the explanation that follows.

A. Algorithm for Subspace Segmentation for Subspaces of Equal and Known Dimensions

The algorithm for subspace segmentation is given in Algorithm 1. We assume that the subspaces have dimension d (for motion segmentation, $d = 4$). The details of the various steps are:

Algorithm 1 Subspace Segmentation

Require: The $m \times N$ data matrix W whose columns are drawn from subspaces of dimension d

Ensure: Clustering of the feature points.

- 1: Compute the SVD of W as in Equation (III.1).
 - 2: Estimate the rank of W (denoted by r) if it is not known. For example, using Equation (III.2) or any other appropriate choice.
 - 3: Compute $(V_r)^t$ consisting of the first r rows of V^t .
 - 4: Normalize the columns of $(V_r)^t$.
 - 5: Replace the data matrix W with $(V_r)^t$.
 - 6: Find the angle between the column vectors of W and represent it as a matrix. {i.e., $\arccos(W^t W)$.}
 - 7: Sort the angles and find the closest neighbors of column vector.
 - 8: **for all** Column vector x_i of W **do**
 - 9: Find the local subspace for the set consisting of x_i and k neighbors (see Equation (III.3)). {Theoretically, k is at least $d-1$. We can use the least square approximation for the subspace (see the section *Local Subspace Estimation*). Let A_i denote the matrix whose columns form an orthonormal bases for the local subspace associated with x_i .}
 - 10: **end for**
 - 11: **for** $i = 1$ to N **do**
 - 12: **for** $j = 1$ to N **do**
 - 13: define $H = (d_{ij}) = (||x_j - A_i^t x_j||_p + ||x_i - A_j^t x_i||_p) / 2$
 - 14: **end for**
 - 15: **end for**{Build the distance matrix}
 - 16: Sort the entries of the $N \times N$ matrix H from smallest to highest values into the vector h and set the threshold η to the value of the T^{th} entry of the sorted and normalized vector h , where T is such that $||\chi_{[T, N^2]} - h||_2$ is minimized, and where $\chi_{[T, N^2]}$ is the characteristic function of the discrete set $[T, N^2]$.
 - 17: Construct a similarity matrix S by setting all entries of H less than threshold η to 1 and by setting all other entries to 0. {Build the binary similarity matrix}
 - 18: Normalize the rows of S using l_1 -norm.
 - 19: Perform SVD $S^t = U_n \Sigma_n (V_n)^t$.
 - 20: Cluster the columns of $\Sigma_n (V_n)^t$ using k-means. $\Sigma_n (V_n)^t$ is the projection on to the span of U_n .
-

Dimensionality Reduction and Normalization: Let W be an $m \times N$ data matrix whose columns are drawn from a union of subspaces of dimensions at most d , possibly perturbed by noise. In order to reduce the dimensionality of the problem, we compute the SVD of W

$$W = U\Sigma V^t \quad (\text{III.1})$$

where $U = [u_1 \ u_2 \ \cdots \ u_m]$ is an $m \times m$ matrix, $V = [v_1 \ v_2 \ \cdots \ v_N]$ is an $N \times N$ matrix, and Σ is an $m \times N$ diagonal matrix with diagonal entries $\sigma_1, \dots, \sigma_l$, where $l = \min\{m, N\}$.

To estimate the effective rank of W , one can use the modal selection algorithm [29] to estimate the rank r if it is not known:

$$r = \operatorname{argmin}_r \frac{\sigma_{r+1}^2}{\sum_{i=1}^r \sigma_i^2} + \kappa r \quad (\text{III.2})$$

where σ_j is the j^{th} singular value and κ is a suitable constant. Another possible model selection algorithm can be found in [31]. $U_r \Sigma_r (V_r)^t$ is the best rank- r approximation of $W = U \Sigma V^t$, where U_r refers to a matrix that has the first r columns of U as its columns and V_r refers to the first r rows of V^t . In the case of motion segmentation, if there are k independent motions across the frames captured by a moving camera, the rank of W is between $2(k+1)$ and $4(k+1)$.

We can now replace the data matrix W with the matrix $(V_r)^t$ that consists of the first r rows of V^t (thereby reducing the dimensionality of data). This step is justified by Proposition 1. Also, [17] discusses the segmentation preserving projections and states that the number of subspaces and their dimensions are preserved by random projections, except for a zero measure set of projections. It should also be noted that this step reduces additive noise as well, especially in the case of light-tailed noise, e.g., Gaussian noise. The number of subspaces corresponds to the number of moving objects. Vidal *et al.* [32] uses an alternative method (power method) for SVD to project incomplete motion data (trajectories) into a 5-dimensional subspace and then applies GPCA and spectral clustering for subspace segmentation. Dimensionality reduction corresponds to Steps 1, 2, and 3 in Algorithm 1.

Another type of data reduction is normalization. Specifically, the columns of $(V_r)^t$ are normalized to lie on the unit sphere \mathbb{S}^{r-1} . This is because by projecting the subspace on the unit sphere, we effectively reduce the dimensionality of the data by one. Moreover, the normalization gives equal contribution of the data matrix columns to the description of the subspaces. Note that the normalization can be done by using l_p norms of the columns of $(V_r)^t$. This normalization procedure corresponds to Steps 4 and 5 in Algorithm 1.

Local Subspace Estimation: The data points (i.e., each column vector of $(V_r)^t$) that are close to each other are likely to belong to the same subspace. For this reason, we estimate a local subspace for each data point using its closest neighbors. This can be done in different ways. For example, if the l_2 -norm is used for normalization, we can find the angles between the points, i.e., we can compute the matrix $\arccos(V_r \times (V_r)^t)$. Then we can sort the angles and find the closest neighbors of each point. If we use l_p -norm for normalization, we can generate a distance matrix $(a_{ij}) = (\|x_i - x_j\|_p)$ and then sort each column of the distance matrix to find the neighbors of each x_i , which is the i^{th} column of $(V_r)^t$.

Once the distance matrix between the points is generated,

we can find, for each point x_i , a set of $k+1 \geq d$ points $\{x_i, x_{i_1}, \dots, x_{i_k}\}$ consisting of x_i and its k closest neighbors. Then we generate a d -dimensional subspace that is nearest (in the least square sense) to the data $\{x_i, x_{i_1}, \dots, x_{i_k}\}$. This is accomplished by using SVD

$$X = [x_i \ x_{i_1} \ \dots \ x_{i_k}] = A \Sigma B^t. \quad (\text{III.3})$$

Let A_i denote the matrix of the first d columns of A associated with x_i . Then, the column space $C(A_i)$ is the d -dimensional subspace nearest to $\{x_i, x_{i_1}, \dots, x_{i_k}\}$. Local subspace estimation corresponds to Steps 6 to 10 in Algorithm 1.

Construction of Binary Similarity Matrix: So far, we have associated a local subspace S_i to each point x_i . Ideally, the points and only those points that belong to the same subspace as x_i should have zero distance from S_i . This suggests computing the distance of each point x_j to the local subspace S_i and forming a distance matrix H .

The distance matrix H is generated as $H = (d_{ij}) = (\|x_j - A_i^t x_j\|_p + \|x_i - A_j^t x_i\|_p) / 2$. A convenient choice of p is 2. Note that as d_{ij} decreases, the probability of having x_j on the same subspace as x_i increases. Moreover, for $p = 2$, $\|x_j - A_i^t x_j\|_2$ is the Euclidean distance of x_j to the subspace associated with x_i .

Since we are not in the ideal case, a point x_j that belongs to the same subspace as x_i may have non-zero distance to S_i . However, this distance is likely to be small compared to the distance between x_j and S_k if x_j and x_k do not belong to the same subspace. This suggests that we compute a threshold that will distinguish between these two cases and transform the distance matrix into a binary matrix in which a zero in the (i, j) entry means x_i and x_j are likely to belong to the same subspace, whereas (i, j) entry of one means x_i and x_j are not likely to belong to the same subspace.

To do this, we convert the distance matrix $H = (d_{ij})_{N \times N}$ into a binary similarity matrix $S = (s_{ij})$. This is done by applying a data-driven thresholding as follows:

- 1) Create a vector h that contains the sorted entries of $H_{N \times N}$ from smallest to highest values. Scale h so that its smallest value is zero and its largest value is one.
- 2) Set the threshold η to the value of the T^{th} entry of the sorted vector h , where T is such that $\|\chi_{[T, N^2]} - h\|_2$ is minimized, and where $\chi_{[T, N^2]}$ is the characteristic function of the discrete set $[T, N^2]$. If the number of points in each subspace are approximately equal, then we would expect about $\frac{N}{n}$ points in each subspace, and we would expect $\frac{N^2}{n^2}$ small entries (zero entries ideally). However, this may not be the case in general. For this reason, we compute the data-driven threshold η that distinguishes the small entries from the large entries.
- 3) Create a similarity matrix S from H such that all entries of H less than the threshold η are set to 1 and the others are set to 0.

The construction of binary similarity corresponds to Steps 11 to 17 in Algorithm 1. In [29], Yan and Pollofeys uses chordal distance (as defined in [33]) between the subspaces $\mathcal{F}(x_i)$ and

$\mathcal{G}(x_j)$ as a measure of the distance between points x_i and x_j

$$d_c^2(\mathcal{F}, \mathcal{G}) = \sum_{i=1}^p \sin^2(\theta_i) \quad (\text{III.4})$$

where $\{\theta_i\}_{i=1}^p$ are the principle angles between p -dimensional local subspaces \mathcal{F} and \mathcal{G} with $\theta_1 \leq \dots \leq \theta_p$. In this approach, the distance between any pairs of points from \mathcal{F} and \mathcal{G} is the same. We find distances between points and local subspaces and our approach distinguishes different points from the same subspace. To see this, let $v \in \text{span}\{Q_{\mathcal{F}}\}$, $\|v\|_2 = 1$, where the columns of $Q_{\mathcal{F}}$ form an orthonormal basis for \mathcal{F} . Thus $v = Q_{\mathcal{F}}x$ for some x with $\|x\|_2 = 1$. Let $Q_{\mathcal{G}}$ form an orthonormal basis for \mathcal{G} , then the Euclidian distance from v to \mathcal{G} squared is given by

$$\begin{aligned} \|v - P_{\mathcal{G}}(v)\|_2^2 &= \|Q_{\mathcal{F}}x - Q_{\mathcal{G}}Q_{\mathcal{G}}^t Q_{\mathcal{F}}x\|_2^2 \\ &= \|x\|_2^2 - x^t Q_{\mathcal{F}}^t Q_{\mathcal{G}} Q_{\mathcal{G}}^t Q_{\mathcal{F}} x \\ &= \|x\|_2^2 - x^t Y \Sigma Z^t Z \Sigma^t Y^t x \\ &= x^t Y Y^t x - x^t Y \Sigma \Sigma^t Y^t x \\ &= x^t Y Y^t x - x^t Y \Sigma^2 Y^t x \\ &= z(I - \Sigma^2)z \end{aligned}$$

where $Y \Sigma Z^t$ is the SVD for $Q_{\mathcal{F}}^t Q_{\mathcal{G}}$ and $z := Y^t x$. Thus, using the relation $\cos \theta_i = \sigma_i$ between principle angles and singular values [34], we get

$$d^2(v, \mathcal{G}) = \sum_{i=1}^p z_i^2 \sin^2(\theta_i). \quad (\text{III.5})$$

Hence, our approach discriminates distances from points in \mathcal{F} to subspace \mathcal{G} . We also have $\sum_{i=1}^p z_i^2 \sin^2(\theta_i) \leq \sum_{i=1}^p \sin^2(\theta_i)$ and therefore d_c is more sensitive to noise.

Using Eq. III.5, we get $0 < \sin \theta_1 \leq d \leq \sin \theta_p$. Assuming a uniform distribution of samples from \mathcal{F} and \mathcal{G} , h can be approximated by a function depicted in Figure III-A. The goal is to find the threshold at the jump discontinuity T from 0 to $\sin \theta_1$. Our method minimizes the highlighted area. Under this model, a simple computation shows that our data driven thresholding algorithm picks $T_d = T$ for $\sin \theta_1 / \sin \theta_p \geq 1/2$, e.g., if $\theta_1 \geq 30^\circ$. In other situations, our algorithm overshoots in estimating the threshold index depending on θ_1 and θ_p .

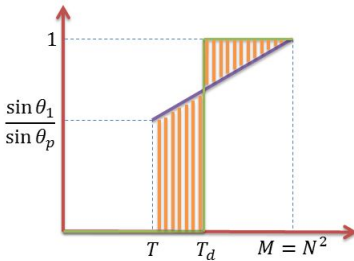


Fig. 1

LINEAR MODELING FOR h

Segmentation: The last step is to use the similarity matrix S to segment the data. To do this, we first normalize the rows of S using l_1 -norm, i.e., $\tilde{S} = D^{-1}S$, where D is a

diagonal matrix $(d_{ij}) = \sum_{j=1}^N s_{ij}$. Note that S and \tilde{S} are not symmetric. \tilde{S} is related to the random walk Laplacian L_r ($\tilde{S} = I - L_r$) [?]. Although other l_p normalizations are possible for $p \geq 1$, however, because of the geometry of the l_1 ball, l_1 -normalization brings outliers closer to the cluster clouds (distances of outliers decrease monotonically as p decreases to 1). Since SVD (which will be used next) is associated with l_2 minimization it is sensitive to outliers. Therefore l_1 normalization works best when SVD is used.

Observe that the initial data segmentation problem has now been converted to segmentation of n 1-dimensional subspaces from the rows of \tilde{S} . This is because, in the ideal case, from the construction of \tilde{S} , if x_i and x_j are in the same subspace, the i^{th} and j^{th} rows of \tilde{S} are equal. Since there are n subspaces, then there will be n 1-dimensional subspaces.

Now, the problem is again a subspace segmentation problem, but this time the data matrix is \tilde{S} with each row as a data point. Also, each subspace is 1-dimensional and there are n subspaces. Therefore, we can apply SVD again to obtain

$$\tilde{S}^t = U_n \Sigma_n (V_n)^t.$$

Using Proposition 1, it can be shown that $\Sigma_n (V_n)^t$ can replace \tilde{S}^t and we cluster the columns of $\Sigma_n (V_n)^t$, which is the projection of \tilde{S} on to the span of U_n . Since the problem is only segmentation of subspaces of dimension 1, we can use any traditional segmentation algorithm such as k-means to cluster the data points. The segmentation corresponds to Steps 18 to 20 in Algorithm 1.

IV. EXPERIMENTAL RESULTS

A. The Hopkins 155 Dataset

The Hopkins 155 Dataset [18] was created as a benchmark database to evaluate motion segmentation algorithms. It contains two (2) and three (3) motion sequences. There are three (3) groups of video sequences in the dataset: (1) 38 sequences of outdoor traffic scenes captured by a moving camera, (2) 104 indoor checker board sequences captured by a handheld camera, and (3) 13 sequences of articulated motions such as head and face motions. Corneriness features that are extracted and tracked across the frames are provided along with the dataset. The ground truth segmentations are also provided for comparison.

B. Results

Tables I, II, and III display some of the experimental results for the Hopkins 155 Dataset. Our Nearness to Local Subspace (NLS) approach have been compared with six (6) motion detection algorithms: (1) GPCA [17], (2) RANSAC [23], (3) Local Subspace Affinity (LSA) [29], (4) MLS [2], [21], (5) Agglomerative Lossy Compression (ALC) [35], and (6) Sparse Subspace Clustering (SSC) [12]. An evaluation of those algorithms is presented in [12] with a minor error in the tabulated results for articulated three motion analysis of SSC-N. SSC-B and SSC-N correspond to Bernoulli and Normal random projections, respectively [12]. The minor error in [12] is the listing of error as 1.42% for articulated three motions.

It is replaced with 1.60% in Table II. In Tables I-III, we used the number of neighbors $k = 3$. Since each point is drawn from a 4-dimensional subspace, a minimum of 3 neighbors are needed to fit a local subspace for each point. Using the same assumption as the algorithms that we compare with, we take the rank of the data matrix to be 8 for two motion and 12 for three motion. Table I displays the misclassification rates for the two motions video sequences. NLS outperforms all of the algorithms for the checkerboard sequences, which are linearly independent motions. The overall misclassification rate is 0.57%. This is 24% better than the next best algorithm. Table II shows the misclassification rates for the three motion sequences. NLS has 1.31% misclassification rate and performs 47% better than the next best algorithm (i.e. SSC-N). Table III presents the misclassification rates for all of the video sequences. Our algorithm NLS (with 0.76% misclassification rate) performs 39% better than the next best algorithm (i.e. SSC-N). In general, our algorithms outperforms SSC-N, which is given as the best algorithm for the two and three motion sequences together.

Table IV shows the performance of the data driven threshold index T_d compared to various other possible thresholds. We provide the results for $\pm 20\%$, $\pm 10\%$, and $\pm 5\%$ deviations from T_d .

Table V displays the robustness of the algorithm with respect to the number of neighbors k . The second portion of the table excludes one pathological sequence from two-motion checker sequence for $k = 4$ and $k = 5$. When k is set to 3 - which is the minimum number of neighbors required - the algorithm performs better.

Table VI displays the increase in the performance of the original LSA algorithm when our distance/similarity and segmentation techniques are applied separately. Both of them improves the performance of the algorithm, however, the new distance and similarity combination contributes more than the new segmentation technique.

Recently, the Low-Rank Representation (LRR) in [15], [16] was applied to the Hopkins 155 Datasets and it generated an error rate of 3.16%. The authors state that this error rate can be reduced to 0.87% by using a variation of LRR with some additional adjustment of a certain parameter.

V. CONCLUSIONS

The NLS approach described in this paper can handle noise effectively, but it works only in special cases of subspaces segmentation problems (i.e., subspaces of equal and known dimensions). Our approach is based on the computation of a binary similarity matrix for the data points. A local subspace is first estimated for each data point. Then, a distance matrix is generated by computing the distances between the local subspaces and points. The distance matrix is converted to the similarity matrix by applying a data-driven threshold. The problem is then transformed to segmentation of subspaces of dimension 1 instead of subspaces of dimension d . The algorithm was applied to the Hopkins 155 Dataset and generated the best results to date.

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<i>Checker (78)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	6.09%	2.57%	6.52%	4.46%	1.55%	0.83%	1.12%	0.23%
Median	1.03%	0.27%	1.75%	0.00%	0.29%	0.00%	0.00%	0.00%
<i>Traffic (31)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	1.41%	5.43%	2.55%	2.23%	1.59%	0.23%	0.02%	1.40%
Median	0.00%	1.48%	0.21%	0.00%	1.17%	0.00%	0.00%	0.00%
<i>Articulated (11)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	2.88%	4.10%	7.25%	7.23%	10.70%	1.63%	0.62%	1.77%
Median	0.00%	1.22%	2.64%	0.00%	0.95%	0.00%	0.00%	0.88%
<i>All (120 seq)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	4.59%	3.45%	5.56%	4.14%	2.40%	0.75%	0.82%	0.57%
Median	0.38%	0.59%	1.18%	0.00%	0.43%	0.00%	0.00%	0.00%

TABLE I

% SEGMENTATION ERRORS FOR SEQUENCES WITH TWO MOTIONS.

<i>Checker (26)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	31.95%	5.80%	25.78%	10.38%	5.20%	4.49%	2.97%	0.87%
Median	32.93%	1.77%	26.00%	4.61%	0.67%	0.54%	0.27%	0.35%
<i>Traffic (7)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	19.83%	25.07%	12.83%	1.80%	7.75%	0.61%	0.58%	1.86%
Median	19.55%	23.79%	11.45%	0.00%	0.49%	0.00%	0.00%	1.53%
<i>Articulated (2)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	16.85%	7.25%	21.38%	2.71%	21.08%	1.60%	1.60%	5.12%
Median	16.85%	7.25%	21.38%	2.71%	21.08%	1.60%	1.60%	5.12%
<i>All (35 seq)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	28.66%	9.73%	22.94%	8.23%	6.69%	3.55%	2.45%	1.31%
Median	28.26%	2.33%	22.03%	1.76%	0.67%	0.25%	0.20%	0.45%

TABLE II

% SEGMENTATION ERRORS FOR SEQUENCES WITH THREE MOTIONS.

<i>All (155 seq)</i>	GPCA	LSA	RANSAC	MSL	ALC	SSC-B	SSC-N	NLS
Average	10.34%	4.94%	9.76%	5.03%	3.56%	1.45%	1.24%	0.76%
Median	2.54%	0.90%	3.21%	0.00%	0.50%	0.00%	0.00%	0.20%

TABLE III

% SEGMENTATION ERRORS FOR ALL SEQUENCES.

<i>All-2 (120 seq)</i>	Data Driven T_d	$0.8T_d$	$0.9T_d$	$0.95T_d$	$1.05T_d$	$1.10T_d$	$1.20T_d$
Average	0.57%	0.95%	1.17%	0.62%	0.58%	1.05%	0.77%
Median	0.00%	0.00%	0.35%	2.27%	2.27%	0.00%	0.00%
<i>All-3 (35 seq)</i>	Data Driven T_d	$0.8T_d$	$0.9T_d$	$0.95T_d$	$1.05T_d$	$1.10T_d$	$1.20T_d$
Average	1.31%	4.39%	3.18%	1.42%	1.20%	1.24%	2.06%
Median	0.45%	0.60%	0.57%	0.46%	0.45%	0.42%	0.37%
<i>All (155 seq)</i>	Data Driven T_d	$0.8T_d$	$0.9T_d$	$0.95T_d$	$1.05T_d$	$1.10T_d$	$1.20T_d$
Average	0.76%	1.84%	1.67%	0.83%	0.74%	1.10%	1.11%
Median	0.20%	0.00%	0.00%	0.20%	0.20%	0.18%	0.19%

TABLE IV

% COMPARISON OF THE DATA DRIVEN THRESHOLD INDEX T_d WITH OTHER CHOICES.

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	<i>ALL SEQ INCLUDED</i>			<i>1 SEQ EXCLUDED</i>	
<i>Checker-2 (78)</i>	k=5	k=4	k=3	k=5	k=4
Average	0.65%	1.59%	0.23%	0.23%	0.97%
Median	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Traffic-2 (31)</i>	k=5	k=4	k=3	k=5	k=4
Average	1.56%	1.66%	1.40%	1.56%	1.66%
Median	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Articulated-2 (11)</i>	k=5	k=4	k=3	k=5	k=4
Average	2.44%	2.33%	1.77%	2.44%	2.33%
Median	0.00%	0.00%	0.88%	0.00%	0.00%
<i>All-2 (120 seq)</i>	k=5	k=4	k=3	k=5	k=4
Average	1.04%	1.75%	0.57%	0.77%	1.35%
Median	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Checker-3 (26)</i>	k=5	k=4	k=3	k=5	k=4
Average	0.44%	0.43%	0.87%	0.44%	0.43%
Median	0.24%	0.22%	0.35%	0.24%	0.22%
<i>Traffic-3 (7)</i>	k=5	k=4	k=3	k=5	k=4
Average	6.59%	7.18%	1.86%	6.59%	7.18%
Median	1.81%	4.37%	1.53%	1.81%	4.37%
<i>Articulated-3 (2)</i>	k=5	k=4	k=3	k=5	k=4
Average	20.54%	4.05%	5.12%	20.54%	4.05%
Median	20.54%	4.05%	5.12%	20.54%	4.05%
<i>All-3 (35 seq)</i>	k=5	k=4	k=3	k=5	k=4
Average	2.82%	1.98%	1.31%	2.82%	1.98%
Median	0.65%	0.47%	0.45%	0.65%	0.47%
<i>All (155 seq)</i>	k=5	k=4	k=3	k=5	k=4
Average	1.50%	1.81%	0.76%	1.30%	1.50%
Median	0.21%	0.00%	0.20%	0.21%	0.00%

TABLE V

% SEGMENTATION ERRORS - NLS ALGORITHM FOR VARIOUS k .

<i>Checker-2 (78)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	2.57%	0.97%	1.71%
Median	0.27%	0.00%	0.00%
<i>Traffic-2 (31)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	5.43%	1.59%	4.99%
Median	1.48%	1.11%	0.65%
<i>Articulated-2 (11)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	4.10%	2.10%	4.26%
Median	1.22%	0.43%	1.21%
<i>All-2 (120 seq)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	3.45%	1.22%	2.27%
Median	0.59%	0.00%	0.35%
<i>Checker-3 (26)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	5.80%	2.66%	4.67%
Median	1.77%	0.30%	0.91%
<i>Traffic-3 (7)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	25.07%	6.38%	24.46%
Median	23.79%	1.28%	31.20%
<i>Articulated-3 (2)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	7.25%	6.18%	7.25%
Median	7.25%	6.18%	7.25%
<i>All-3 (35 seq)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	9.73%	2.45%	8.78%
Median	2.33%	0.20%	1.94%
<i>All (155 seq)</i>	LSA(Original)	LSA(New Dist/Similarity)	LSA(New Segmentation)
Average	4.94%	1.84%	3.96%
Median	0.90%	0.18%	0.61%

TABLE VI

% SEGMENTATION ERRORS FOR LSA WITH VARIOUS PARAMETERS.